

Sub B1  
92. (New) A recombinant host cell comprising the isolated polynucleotide of claim 86.

### Remarks

The attached Substitute Sequence Listing has been prepared in response to a Notice To Comply With Requirements For Patent Applications Containing Nucleotide Sequence And/Or Amino Acid Sequence Disclosures (Paper No. 8) mailed January 14, 2003. Two new sequences (SEQ ID NOS: 453 and 454) have been added which correspond to the consensus amino acid sequences disclosed in the specification at pages 10 and 11. The corresponding references to the sequence listing have been added to the specification at pages 10 and 11. The remainder of the Substitute Sequence Listing is identical in content to the previous sequence listing. No new matter has been introduced.

The specification also has been amended to include the priority claim of the present application pursuant to 37 C.F.R. § 1.78(a). Claims 1-9 and 13 have been canceled without prejudice or disclaimer. New claims 22-92 have been added in order to claim additional embodiments of the subject matter of the provisionally-elected group and provisionally-elected polynucleotides. The new claims make reference to the sequence listing where appropriate. Thus, the concern expressed in the Notice To Comply (Paper No. 8) that the claims do not comply with C.F.R. § 1.821(d) has been obviated.

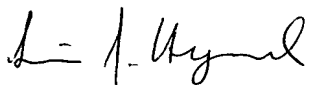
New claims 22-92 find support throughout the specification and claims as originally filed. Specifically, support for new claims 22-24, 74, and 79-81 is found, for example, at page 3, lines 15-23; at page 4, lines 6-13; at page 11, lines 13-18; and at page 12, lines 28-38. Support for new claims 25, 40, 53, 65, 75, 82, and 90 is found, for example, at page 12, lines 18-27; and at page 18, lines 15-18. Support for new claims 26, 41, 54, and 66 is found, for example, at page 14, line 29 through page 15, line 14. Support for new claims 27, 42, 55, 67, 76, 83, and 90 is found, for example, in Example 1 at page 41, line 26 through page 42, line 31. Support for new claims 28, 43, 56, 68, 77, 84, and 91 is found, for example, at page 12, lines 18-21; at page 18, lines 15-18; and at page 18, line 25 through page 20, line 3. Support for new claims 29-31, 44-46, 57-59, 69-71, 78, 85, and 92 is found, for example, at page 12, lines 21-24; at page 18, lines 15-18; and at page 18, line 25 through page 20, line 8. Support for new claims 32, 47, 60, and 72 is found, for example, at page 22, lines 6-12. Support for new claims 33, 48, 61,

and 73 is found, for example, at page 21, lines 23-33, and at page 22, lines 4-12. Support for new claims 34-39 is found, for example, at page 23, lines 24-38; at page 24, lines 1-19; and in Tables 1 and 2. Support for new claims 49-52 is found, for example, at page 24, line 37 through page 25, line 8. Support for new claims 62-64 is found, for example, at page 3, lines 24-35; at page 12, lines 15-17; and at page 13, lines 29-38. Support for new claims 86-88 is found, for example, at page 13, lines 7-14. Thus, no new matter has been added by way of amendment.

Claims 10-12, 14-21, and 22-92 will be pending upon entry of this amendment.

Respectfully submitted,

Date: 14 February 2003

  
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Lin J. Hymel (Reg. No. 45,414)  
Attorney for Applicants

Human Genome Sciences, Inc.  
9410 Key West Avenue  
Rockville, MD 20850  
(301) 251-6015 (telephone)

KKH/MJH/LJH/rmr



VIA HAND DELIVERY February 14, 2003

**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

Application of: Choi et al.

Group Art Unit: 1645

Application Number: 09/765,272

Examiner: Duffy, P.

Filed: January 22, 2001

Atty. Docket No.: PB340P2C2

Title: *Streptococcus pneumoniae* Antigens and Vaccines

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**Version With Markings To Show Changes Made**

TECH CENTER 1600/2900

The paragraph at page 10, lines 31-36, has been amended as follows:

3. *Lipoprotein*: Studies of the cleavage sites of twenty-six bacterial lipoprotein precursors has allowed the definition of a consensus amino acid sequence for lipoprotein cleavage. Nearly three-fourths of the bacterial lipoprotein precursors examined contained the sequence L-(A,S)-(G,A)-C (SEQ ID NO:453) at positions -3 to +1, relative to the point of cleavage (Hayashi, S. and Wu, H. C., *J. Bioenerg. Biomembr.* **22**:451-471 (1990)).

The paragraph at page 10, line 37 through page 11, line 10, has been amended as follows:

4. *LPXTG motif*: It has been experimentally determined that most anchored proteins found on the surface of gram-positive bacteria possess a highly conserved carboxy terminal sequence. More than fifty such proteins from organisms such as *S. pyogenes*, *S. mutans*, *E. faecalis*, *S. pneumoniae*, and others, have been identified based on their extracellular location and carboxy terminal amino acid sequence (Fischetti, V. A., *ASM News* **62**:405-410 (1996)). The conserved region consists of six charged amino acids at the extreme carboxy terminus coupled to 15-20 hydrophobic amino acids presumed to function as a transmembrane domain. Immediately adjacent to the transmembrane domain is a six amino acid sequence conserved in nearly all proteins examined. The amino acid sequence of this region is L-P-X-T-G-X (SEQ ID NO:454), where X is any amino acid.